

LH 5630



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/926,820

DATE: 06/06/2002

TIME: 12:57:55

Input Set : A:\10496431.app

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ENTERED

3 <110> APPLICANT: FORSSMANN, WOLF-GEORG
 4 MAGERT, HANS-JURGEN
 5 STANDKER, LUDGER
 6 KREUTZMANN, PETER
 8 <120> TITLE OF INVENTION: SERINE PROTEASE INHIBITORS
 10 <130> FILE REFERENCE: 10496-P67431US0
 12 <140> CURRENT APPLICATION NUMBER: 09/926,820
 C--> 13 <141> CURRENT FILING DATE: 2002-05-06
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP99/04331
 16 <151> PRIOR FILING DATE: 1999-06-22
 18 <160> NUMBER OF SEQ ID NOS: 12
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1064
 24 <212> TYPE: PRT
 25 <213> ORGANISM: mammalian
 27 <400> SEQUENCE: 1
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 29 1 5 10 15
 31 Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
 32 20 25 30
 34 Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
 35 35 40 45
 37 Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
 38 50 55 60
 40 Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
 41 65 70 75 80
 43 Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
 44 85 90 95
 46 Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
 47 100 105 110
 49 Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
 50 115 120 125
 52 Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
 53 130 135 140
 55 Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val
 56 145 150 155 160
 58 Cys Ser Ala Phe Arg Pro Phe Val Arg Asp Gly Arg Leu Gly Cys Thr
 59 165 170 175
 61 Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn
 62 180 185 190
 64 Lys Cys Ala Met Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala
 65 195 200 205

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67 Lys Arg Glu Gly Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe
68      210      215      220
70 Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr
71 225      230      235      240
73 Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn
74      245      250      255
76 Lys Cys Ala Leu Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu
77      260      265      270
79 Asn Ser Lys Thr Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys
80      275      280      285
82 Val Lys Arg Glu Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala
83      290      295      300
85 Lys Asn Gly Ile Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly
86 305      310      315      320
88 Pro Asp Gly Lys Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr
89      325      330      335
91 Phe Gln Ala Glu Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg
92      340      345      350
94 Asn Lys Arg Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn
95      355      360      365
97 Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu
98      370      375      380
100 Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys
101 385      390      395      400
103 Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys
104      405      410      415
106 Lys Glu Gly Glu Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser
107      420      425      430
109 Phe Glu Glu Leu Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg
110      435      440      445
112 Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys
113      450      455      460
115 Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu
116 465      470      475      480
118 Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys
119      485      490      495
121 Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg
122      500      505      510
124 Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys
125      515      520      525
127 Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Glu Glu Glu Lys Lys
128      530      535      540
130 Asn Asp Lys Glu Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg
131 545      550      555      560
133 Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn
134      565      570      575
136 Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp
137      580      585      590
139 Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln

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140          595          600          605
142 Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys
143          610          615          620
145 Arg Glu Ala Glu Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln
146 625          630          635          640
148 Asn Gly Lys Leu Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro
149          645          650          655
151 Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe
152          660          665          670
154 Gln Lys Glu Asn Glu Glu Arg Lys Arg Lys Glu Glu Glu Asp Gln Arg
155          675          680          685
157 Asn Ala Ala Gly His Gly Ser Ser Gly Gly Gly Gly Asn Thr Gln
158          690          695          700
160 Asp Glu Cys Ala Glu Tyr Gln Glu Gln Met Lys Asn Gly Arg Leu Ser
161 705          710          715          720
163 Cys Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr
164          725          730          735
166 Asn Asn Gln Cys Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu
167          740          745          750
169 Arg Lys Asn Glu Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu
170          755          760          765
172 Ser Gly Lys Asp Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly
173          770          775          780
175 Lys Leu Ile Cys Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly
176 785          790          795          800
178 Lys Thr His Gly Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg
179          805          810          815
181 Glu Ala Ala Glu Lys Lys Lys Lys Glu Asp Glu Asp Arg Ser Asn Thr
182          820          825          830
184 Gly Glu Arg Ser Asn Thr Gly Glu Arg Ser Asn Asp Lys Glu Asp Leu
185          835          840          845
187 Cys Arg Glu Phe Arg Ser Met Gln Arg Asn Gly Lys Leu Ile Cys Thr
188          850          855          860
190 Arg Glu Asn Asn Pro Val Arg Gly Pro Tyr Gly Lys Met His Ile Asn
191 865          870          875          880
193 Lys Cys Ala Met Cys Gln Ser Ile Phe Asp Arg Glu Ala Asn Glu Arg
194          885          890          895
196 Lys Lys Lys Asp Glu Glu Lys Ser Ser Ser Lys Pro Ser Asn Asn Ala
197          900          905          910
199 Lys Asp Glu Cys Ser Glu Phe Arg Asn Tyr Ile Arg Asn Asn Glu Leu
200          915          920          925
202 Ile Cys Pro Arg Glu Asn Asp Pro Val His Gly Ala Asp Gly Lys Phe
203          930          935          940
205 Tyr Thr Asn Lys Cys Tyr Met Cys Arg Ala Val Phe Leu Thr Glu Ala
206 945          950          955          960
208 Leu Glu Arg Ala Lys Leu Gln Glu Lys Pro Ser His Val Arg Ala Ser
209          965          970          975
211 Gln Glu Glu Asp Ser Pro Asp Ser Phe Ser Ser Leu Asp Ser Glu Met
212          980          985          990

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214 Cys Lys Asp Tyr Arg Val Leu Pro Arg Ile Gly Tyr Leu Cys Pro Lys
215          995          1000          1005
217 Asp Leu Lys Pro Val Cys Gly Asp Asp Gly Gln Thr Tyr Asn Asn Pro
218    1010          1015          1020
220 Cys Met Leu Cys His Glu Asn Leu Ile Arg Gln Thr Asn Thr His Ile
221 1025          1030          1035          1040
223 Arg Ser Thr Gly Lys Cys Glu Glu Ser Ser Thr Pro Gly Thr Thr Ala
224          1045          1050          1055
226 Ala Ser Met Pro Pro Ser Asp Glu
227          1060
230 <210> SEQ ID NO: 2
231 <211> LENGTH: 35
232 <212> TYPE: PRT
233 <213> ORGANISM: mammalian
235 <400> SEQUENCE: 2
236 Ser Ala Phe Arg Pro Phe Val Arg Asp Gly Arg Leu Gly Cys Thr Arg
237   1          5          10          15
239 Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn Lys
240          20          25          30
242 Cys Ala Met
243          35
246 <210> SEQ ID NO: 3
247 <211> LENGTH: 35
248 <212> TYPE: PRT
249 <213> ORGANISM: mammalian
251 <400> SEQUENCE: 3
252 Asn Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg
253   1          5          10          15
255 Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr
256          20          25          30
258 Cys Ser Met
259          35
262 <210> SEQ ID NO: 4
263 <211> LENGTH: 35
264 <212> TYPE: PRT
265 <213> ORGANISM: mammalian
267 <400> SEQUENCE: 4
268 Arg Glu Phe Arg Ser Met Gln Arg Asn Gly Lys Leu Ile Cys Thr Arg
269   1          5          10          15
271 Glu Asn Asn Pro Val Arg Gly Pro Tyr Gly Lys Met His Ile Asn Lys
272          20          25          30
274 Cys Ala Met
275          35
278 <210> SEQ ID NO: 5
279 <211> LENGTH: 35
280 <212> TYPE: PRT
281 <213> ORGANISM: mammalian
283 <400> SEQUENCE: 5
284 Ser Glu Phe Arg Asn Tyr Ile Arg Asn Asn Glu Leu Ile Cys Pro Arg

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285      1              5              10              15
287 Glu Asn Asp Pro Val His Gly Ala Asp Gly Lys Phe Tyr Thr Asn Lys
288              20              25              30
290 Cys Tyr Met
291              35
294 <210> SEQ ID NO: 6
295 <211> LENGTH: 52
296 <212> TYPE: PRT
297 <213> ORGANISM: mammalian
299 <400> SEQUENCE: 6
300 Lys Asp Tyr Arg Val Leu Pro Arg Ile Gly Tyr Leu Cys Pro Lys Asp
301      1              5              10              15
303 Leu Lys Pro Val Cys Gly Asp Asp Gly Gln Thr Tyr Asn Asn Pro Cys
304              20              25              30
306 Met Leu Cys His Glu Asn Leu Ile Arg Gln Thr Asn Thr His Ile Arg
307              35              40              45
309 Ser Thr Gly Lys
310              50
313 <210> SEQ ID NO: 7
314 <211> LENGTH: 3532
315 <212> TYPE: DNA
316 <213> ORGANISM: mammalian
318 <220> FEATURE:
319 <221> NAME/KEY: CDS
320 <222> LOCATION: (44)..(3235)
322 <400> SEQUENCE: 7
323 tatgcatgga gtggacctgt aggcgacttg catcgtcttc aac atg aag ata gcc      55
324                               Met Lys Ile Ala
325                               1
327 aca gtg tca gtg ctt ctg ccc ttg gct ctt tgc ctc ata caa gat gct      103
328 Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu Ile Gln Asp Ala
329      5              10              15              20
331 gcc agt aag aat gaa gat cag gaa atg tgc cat gaa ttt cag gca ttt      151
332 Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe
333              25              30              35
335 atg aaa aat gga aaa ctg ttc tgt ccc cag gat aag aaa ttt ttt caa      199
336 Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln
337              40              45              50
339 agt ctt gat gga ata atg ttc atc aat aaa tgt gcc acg tgc aaa atg      247
340 Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met
341              55              60              65
343 ata ctg gaa aaa gaa gca aaa tca cag aag agg gcc agg cat tta gca      295
344 Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala Arg His Leu Ala
345              70              75              80
347 aga gct ccc aag gct act gcc cca aca gag ctg aat tgt gat gat ttt      343
348 Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn Cys Asp Asp Phe
349      85              90              95              100
351 aaa aaa gga gaa aga gat ggg gat ttt atc tgt cct gat tat tat gaa      391
352 Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro Asp Tyr Tyr Glu

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VERIFICATION SUMMARY

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